SEQUENCE LISTING

<110> Allan, Bernard
Lavan, Brian
Moodie, Shonna
Waters, Steve
Wong, Chi-Wai
Metabolex, Inc.

<120> Methods of Diagnosing & Treating Diabetes and Insulin Resistance

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<141> 2004-12-02

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Lys Pro Trp Ser Gly Ile Ser Val Tyr Met Phe Asn Leu Ala Leu Ala
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Asp Phe Leu Tyr Val Leu Thr Leu Pro Ala Leu Ile Phe Tyr Tyr Phe
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Asn Lys Thr Asp Trp Ile Phe Gly Asp Ala Met Cys Lys Leu Gln Arg
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Phe Ile Phe His Val Asn Leu Tyr Gly Ser Ile Leu Phe Leu Thr Cys
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Gly Phe Leu Gly Asn Ser Val Ala Ile Trp Met Phe Val Phe His Met
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Lys Pro Trp Ser Gly Ile Ser Val Tyr Met Phe Asn Leu Ala Leu Ala
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Lys Ser Ile Tyr Leu Val Ile Ile Val Leu Thr Val Phe Ala Val Ser
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Tyr Ile Pro Phe His Val Met Lys Thr Met Asn Leu Arg Ala Arg Leu
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(PTPLA)

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35 40 45

Ser Asp Glu Lys Glu Ala Ala Gly Lys Arg Arg Arg Leu Gly Leu Leu
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Ala Thr Ala Trp Leu Thr Phe Tyr Asn Ile Ala Met Thr Ala Gly Trp
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Leu Val Leu Ala Ile Ala Met Val Arg Phe Tyr Met Glu Lys Gly Thr
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Val Val Leu Phe Leu Val Ser Trp Thr Val Thr Glu Ile Thr Arg Tyr
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Ser Phe Tyr Thr Phe Ser Leu Leu Asp His Leu Pro His Phe Ile Lys
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Trp Ala Arg Tyr Asn Leu Phe Ile Ile Leu Tyr Pro Val Gly Val Ala
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Gly Glu Leu Leu Thr Ile Tyr Ala Ala Leu Pro Tyr Val Lys Lys Ser
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Gly Met Phe Ser Val Arg Leu Pro Asn Lys Tyr Asn Val Ser Phe Asp
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Tyr Tyr Tyr Phe Leu Leu Ile Thr Met Ala Ser Tyr Ile Pro Leu Phe
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Thr Cys Ala Ser Gln Arg Asn Glu Ser Cys Gly Gly Thr Phe Gly Ile
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Tyr Gly Thr Cys Asp Arg Gly Leu Arg Cys Val Ile Arg Pro Pro Leu
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Asn Gly Asp Ser Leu Thr Glu Tyr Glu Ala Gly Val Cys Glu Asp Glu
            100                 105                 110

Asn Trp Thr Asp Asp Gln Leu Leu Gly Phe Lys Pro Cys Asn Glu Asn
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Leu Ile Ala Gly Cys Asn Ile Ile Asn Gly Lys Cys Glu Cys Asn Thr
    130                 135                 140
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Leu Ser Ala Leu Lys Arg Ile Glu Glu Glu Lys Pro Asp Cys Ser Lys
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Ala Arg Cys Glu Val Gln Phe Ser Pro Arg Cys Pro Glu Asp Ser Val
            180                 185                 190

Leu Ile Glu Gly Tyr Ala Pro Pro Gly Glu Cys Cys Pro Leu Pro Ser
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Arg Cys Val Cys Asn Pro Ala Gly Cys Leu Arg Lys Val Cys Gln Pro
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Gly Asn Leu Asn Ile Leu Val Ser Lys Ala Ser Gly Lys Pro Gly Glu
225                 230                 235                 240

Cys Cys Asp Leu Tyr Glu Cys Lys Pro Val Phe Gly Val Asp Cys Arg
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Thr Val Glu Cys Pro Pro Val Gln Gln Thr Ala Cys Pro Pro Asp Ser
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Tyr Glu Thr Gln Val Arg Leu Thr Ala Asp Gly Cys Cys Thr Leu Pro
        275                 280                 285

Thr Arg Cys Glu Cys Leu Ser Gly Leu Cys Gly Phe Pro Val Cys Glu
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Val Gly Ser Thr Pro Arg Ile Val Ser Arg Gly Asp Gly Thr Pro Gly
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Lys Cys Cys Asp Val Phe Glu Cys Val Asn Asp Thr Lys Pro Ala Cys
                325                 330                 335

Val Phe Asn Asn Val Glu Tyr Tyr Asp Gly Asp Met Phe Arg Met Asp
            340                 345                 350

Asn Cys Arg Phe Cys Arg Cys Gln Gly Gly Val Ala Ile Cys Phe Thr
        355                 360                 365

Ala Gln Cys Gly Glu Ile Asn Cys Glu Arg Tyr Tyr Val Pro Glu Gly
    370                 375                 380

Glu Cys Cys Pro Val Cys Glu Asp Pro Val Tyr Pro Phe Asn Asn Pro
385                 390                 395                 400

Ala Gly Cys Tyr Ala Asn Gly Leu Ile Leu Ala His Gly Asp Arg Trp
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Arg Glu Asp Asp Cys Thr Phe Cys Gln Cys Val Asn Gly Glu Arg His
            420                 425                 430

Cys Val Ala Thr Val Cys Gly Gln Thr Cys Thr Asn Pro Val Lys Val
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Pro Gly Glu Cys Cys Pro Val Cys Glu Glu Pro Thr Ile Ile Thr Val
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Gln Cys Ile Asn Thr Glu Glu Leu Cys Ser Glu Arg Lys Gln Gly Cys
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Thr Leu Asn Cys Pro Phe Gly Phe Leu Thr Asp Ala Gln Asn Cys Glu
        515                 520                 525

Ile Cys Glu Cys Arg Pro Arg Pro Lys Lys Cys Arg Pro Ile Ile Cys
    530                 535                 540

Asp Lys Tyr Cys Pro Leu Gly Leu Leu Lys Asn Lys His Gly Cys Asp
545                 550                 555                 560

Ile Cys Arg Cys Lys Lys Cys Pro Glu Leu Ser Cys Ser Lys Ile Cys
                565                 570                 575

Pro Leu Gly Phe Gln Gln Asp Ser His Gly Cys Leu Ile Cys Lys Cys
            580                 585                 590

Arg Glu Ala Ser Ala Ser Ala Gly Pro Pro Ile Leu Ser Gly Thr Cys
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Leu Thr Val Asp Gly His His His Lys Asn Glu Glu Ser Trp His Asp
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Gly Cys Arg Glu Cys Tyr Cys Leu Asn Gly Arg Glu Met Cys Ala Leu
625                 630                 635                 640

Ile Thr Cys Pro Val Pro Ala Cys Gly Asn Pro Thr Ile His Pro Gly
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Gln Cys Cys Pro Ser Cys Ala Asp Asp Phe Val Val Gln Lys Pro Glu
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Leu Ser Thr Pro Ser Ile Cys His Ala Pro Gly Gly Glu Tyr Phe Val
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Glu Gly Glu Thr Trp Asn Ile Asp Ser Cys Thr Gln Cys Thr Cys His
    690                 695                 700

Ser Gly Arg Val Leu Cys Glu Thr Glu Val Cys Pro Pro Leu Leu Cys
705                 710                 715                 720

Gln Asn Pro Ser Arg Thr Gln Asp Ser Cys Cys Pro Gln Cys Thr Asp
                725                 730                 735

Gln Pro Phe Arg Pro Ser Leu Ser Arg Asn Asn Ser Val Pro Asn Tyr
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Cys Lys Asn Asp Glu Gly Asp Ile Phe Leu Ala Ala Glu Ser Trp Lys
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Pro Asp Val Cys Thr Ser Cys Ile Cys Ile Asp Ser Val Ile Ser Cys
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Val Val Cys His Phe Ser Gly Lys Ala Tyr Ala Asp Glu Glu Arg Trp
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Asp Leu Asp Ser Cys Thr His Cys Tyr Cys Leu Gln Gly Gln Thr Leu
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Cys Ser Thr Val Ser Cys Pro Pro Leu Pro Cys Val Glu Pro Ile Asn
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Val Glu Gly Ser Cys Cys Pro Met Cys Pro Glu Met Tyr Val Pro Glu
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Pro Thr Asn Ile Pro Ile Glu Lys Thr Asn His Arg Gly Glu Val Asp
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Leu Pro Arg Asp Met Gly His Leu Gln Val Asp Tyr Arg Asp Asn Arg
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Leu His Pro Ser Glu Asp Ser Ser Leu Asp Ser Ile Ala Ser Val Val
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Val Pro Ile Ile Ile Cys Leu Ser Ile Ile Ile Ala Phe Leu Phe Ile
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Asn Gln Lys Lys Gln Trp Ile Pro Leu Leu Cys Trp Tyr Arg Thr Pro
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Thr Lys Pro Ser Ser Leu Asn Asn Gln Leu Val Ser Val Asp Cys Lys
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Lys Gly Thr Arg Val Gln Val Asp Ser Ser Gln Arg Met Leu Arg Ile
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<210> 14
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<212> PRT
<213> Mus musculus

<220>
<223> mouse cysteine-rich repeat-containing protein,
cysteine-rich motorneuron 1 (CRIM1), partial

<400> 14
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20 25 30

Glu Ser Lys Cys Glu Glu Pro Arg Ser Cys Pro Gly Ser Ile Val Gln
35 40 45

Gly Val Cys Gly Cys Cys Tyr Met Cys Ala Arg Gln Arg Asn Glu Ser
50 55 60

Cys Gly Gly Ala Tyr Gly Leu His Gly Ala Cys Asp Arg Gly Leu Arg
65 70 75 80

Cys Val Ile Arg Pro Pro Leu Asn Gly Asp Ser Ile Thr Glu Tyr Glu
85 90 95

Val Gly Val Cys Glu Asp Glu Asp Trp Asp Asp Asp Gln Leu Ile Gly
100 105 110

Phe Glu Pro Cys Asn Glu Asn Leu Ile Ser Gly Cys Asn Ile Ile Asn
115 120 125

Gly Lys Cys Glu Cys Gly Thr Ile Arg Thr Cys Asn Asn Pro Phe Glu
130 135 140

Phe Pro Arg Lys Asp Met Cys Leu Ser Ala Leu Lys Arg Ile Glu Glu
145 150 155 160

Glu Lys Pro Asp Cys Ser Lys Ala Arg Cys Glu Val Arg Phe Ser Pro
165 170 175

```
Arg Cys Pro Glu Asp Ser Ile Leu Ile Glu Gly Tyr Ala Pro Pro Gly
            180                 185                 190

Glu Cys Cys Pro Leu Pro Ser Arg Cys Val Cys Asp Pro Ala Gly Cys
        195                 200                 205

Leu Arg Lys Val Cys Gln Pro Gly Tyr Leu Asn Ile Leu Val Ser Lys
    210                 215                 220

Ala Ser Gly Lys Pro Gly Glu Cys Cys Asp Leu Tyr Glu Cys Lys Pro
225                 230                 235                 240

Val Phe Ser Val Asp Cys Ser Thr Val Glu Cys Pro Pro Val Gln Gln
                245                 250                 255

Ala Val Cys Pro Leu Asp Ser Tyr Glu Thr Gln Val Arg Leu Thr Ala
            260                 265                 270

Asp Gly Cys Cys Thr Leu Pro Ala Arg Cys Glu Cys Leu Ser Gly Leu
        275                 280                 285

Cys Gly Phe Pro Val Cys Glu Val Gly Ser Thr Pro Arg Ile Val Ser
    290                 295                 300

Arg Gly Asp Gly Thr Pro Gly Lys Cys Cys Asp Val Phe Glu Cys Val
305                 310                 315                 320

Asn Glu Thr Lys Pro Ala Cys Val Phe Asn Ser Val Glu Tyr Tyr Asp
                325                 330                 335

Gly Asp Met Phe Arg Met Asp Asn Cys Arg Phe Cys Arg Cys Gln Gly
            340                 345                 350

Gly Val Ser Ile Cys Phe Thr Ala Gln Cys Gly Glu Leu Asn Cys Glu
        355                 360                 365

Arg Tyr Tyr Val Pro Glu Gly Glu Cys Cys Pro Val Cys Glu Asp Pro
    370                 375                 380

Ile Tyr Pro Leu Asn Asn Pro Ala Gly Cys Tyr Ala Asn Gly Gln Ile
385                 390                 395                 400

Arg Ala His Gly Asp Arg Trp Arg Glu Asp Asp Cys Thr Phe Cys Gln
                405                 410                 415

Cys Ile Asn Gly Glu Pro His Cys Val Ala Thr Ala Cys Gly Gln Ser
            420                 425                 430

Cys Met His Pro Val Lys Val Pro Gly Glu Cys Cys Pro Val Cys Glu
        435                 440                 445

Glu Pro Thr Tyr Ile Thr Ile Asp Pro Pro Ala Cys Gly Glu Leu Ser
    450                 455                 460

Asn Cys Ser Leu Lys Glu Lys Asp Cys Val Tyr Gly Phe Lys Leu Asp
465                 470                 475                 480

His Asn Gly Cys Arg Thr Cys Gln Cys Lys Ile Arg Glu Glu Leu Cys
                485                 490                 495
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Leu Gly Leu Lys Arg Ala Cys Thr Leu Asp Cys Pro Phe Gly Phe Leu
500 505 510

Thr Asp Val His Asn Cys Glu Leu Cys Gln Cys Arg Pro Arg Pro Lys
515 520 525

Lys Cys Arg Pro Thr Met Cys Asp Lys Phe Cys Pro Leu Gly Phe Leu
530 535 540

Lys Asn Lys His Gly Cys Asp Ile Cys Arg Cys Lys Lys Cys Pro Glu
545 550 555 560

Leu Pro Cys Ser Lys Ile Cys Pro Leu Gly Phe Gln Gln Asp Ser His
565 570 575

Gly Cys Leu Ile Cys Lys Cys Arg Glu Val Pro Pro Ser Ala Gly Pro
580 585 590

Pro Val Leu Ser Gly Thr Cys Leu Ser Met Asp Gly His His His Lys
595 600 605

Asn Glu Glu Ser Trp His Asp Gly Cys Arg Glu Cys Tyr Cys His Asn
610 615 620

Gly Lys Glu Met Cys Ala Leu Ile Thr Cys Pro Val Pro Ala Cys Gly
625 630 635 640

Asn Pro Thr Ile Arg Ser Gly Gln Cys Cys Pro Ser Cys Thr Asp Asp
645 650 655

Phe Val Val Gln Lys Pro Glu Leu Ser Thr Pro Ser Ile Cys His Ala
660 665 670

Pro Gly Gly Glu Tyr Phe Val Glu Gly Glu Thr Trp Asn Ile Asp Ser
675 680 685

Cys Thr Gln Cys Thr Cys His Ser Gly Arg Val Leu Cys Glu Thr Glu
690 695 700

Val Cys Pro Pro Leu Leu Cys Gln Asn Pro Ser Arg Thr Gln Asp Ser
705 710 715 720

Cys Cys Pro Gln Cys Thr Asp Asp Pro Pro Gln Pro Ser Thr Ser His
725 730 735

Asn Glu Ser Val Pro Ser Tyr Cys Arg Asn Asp Glu Gly Asp Ile Phe
740 745 750

Leu Ala Ala Glu Ser Trp Lys Pro Asp Ala Cys Thr Ser Cys Val Cys
755 760 765

Val Asp Ser Ala Ile Ser Cys Tyr Ser Glu Ser Cys Pro Ser Val Ala
770 775 780

Cys Glu Arg Pro Val Leu Arg Lys Gly Gln Cys Cys Pro Tyr Cys Leu
785 790 795 800

Glu Asp Thr Ile Pro Lys Lys Val Val Cys His Phe Ser Gly Lys Thr
805 810 815

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Tyr Ala Asp Glu Glu Arg Trp Asp Ile Asp Ser Cys Thr His Cys Tyr
            820                 825                 830

Cys Leu Gln Gly Gln Thr Leu Cys Ser Thr Val Ser Cys Pro Pro Leu
        835                 840                 845

Pro Cys Ala Glu Pro Ile Lys Val Glu Gly Ser Cys Cys Pro Met Cys
    850                 855                 860

Pro Glu Met Tyr Val Pro Glu Pro Thr Asn Val Pro Ile Glu Lys Lys
865                 870                 875                 880

Asn His Arg Gly Glu Ile Asp Leu Glu Val Pro Met Trp Pro Thr Pro
                885                 890                 895

Ser Glu Asn Asp Ile Ile His Leu Pro Arg Asp Met Gly His Leu Gln
            900                 905                 910

Val Asp Tyr Arg Asp Asn Asn Arg Leu His Pro Gly Glu Asp Ser Ser
        915                 920                 925

Leu Asp Ser Ile Val Ser Val Val Val Pro Ile Ile Ile Cys Leu Ser
    930                 935                 940

Ile Ile Ile Ala Phe Leu Leu Ile Asn Gln Lys Lys Gln Trp Val Pro
945                 950                 955                 960

Leu Leu Cys Trp Tyr Arg Thr Pro Thr Lys Pro Ser Ser Leu Asn Asn
                965                 970                 975

Gln Leu Val Ser Val Asp Cys Lys Lys Gly Thr Arg Val Gln Val Asp
            980                 985                 990

Gly Pro Gln Arg Met Leu Arg Ile Ala Glu Pro Asp Ala Arg Phe Ser
        995                1000                1005

Gly Phe Tyr Ser Met Gln Lys Gln Asn His Leu Gln Ala Asp Asn Phe
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Tyr Gln Thr Val
1025
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<210> 15
<211> 2276
<212> DNA
<213> Homo sapiens

<220>
<223> human calmodulin-dependent phosphoprotein
phosphatase catalytic subunit, calcineurin A alpha
(PPP3CA) cDNA

<220>
<221> CDS
<222> (148)..(1713)
<223> PPP3CA

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gcggcgttga gtgtctggcc cgccggtccg gtcggggtgt gcagtcggac ggacgagcag 120

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aaggagggaa ggctggaaga gagtgttgca ttgagaataa taacagaggg tgcatcaatt 360
cttcgacagg aaaaaaattt gctggatatt gatgcgccag tcactgtttg tggggacatt 420
catggacaat tctttgattt gatgaagctc tttgaagtcg ggggatctcc tgccaacact 480
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tatttgtggg ccttgaaaat tctctacccc aaaacactgt ttttacttcg tggaaatcat 600
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gaacgagtat atgatgcctg tatggatgcc tttgactgcc ttcccctggc tgccctgatg 720
aaccaacagt tcctgtgtgt gcatggtggt ttgtctccag agattaacac tttagatgat 780
atcagaaaat tagaccgatt caaagaacca cctgcatatg gacctatgtg tgatatcctg 840
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<210> 16
<211> 521
<212> PRT
<213> Homo sapiens

<220>
<223> human calmodulin-dependent phosphoprotein
phosphatase catalytic subunit, calcineurin A alpha
(PPP3CA)

<400> 16

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Met Ser Glu Pro Lys Ala Ile Asp Pro Lys Leu Ser Thr Thr Asp Arg
  1               5                  10                  15

Val Val Lys Ala Val Pro Phe Pro Pro Ser His Arg Leu Thr Ala Lys
            20                  25                  30

Glu Val Phe Asp Asn Asp Gly Lys Pro Arg Val Asp Ile Leu Lys Ala
        35                  40                  45

His Leu Met Lys Glu Gly Arg Leu Glu Glu Ser Val Ala Leu Arg Ile
    50                  55                  60
```

```
Ile Thr Glu Gly Ala Ser Ile Leu Arg Gln Glu Lys Asn Leu Leu Asp
 65                  70                  75                  80

Ile Asp Ala Pro Val Thr Val Cys Gly Asp Ile His Gly Gln Phe Phe
                85                  90                  95

Asp Leu Met Lys Leu Phe Glu Val Gly Gly Ser Pro Ala Asn Thr Arg
            100                 105                 110

Tyr Leu Phe Leu Gly Asp Tyr Val Asp Arg Gly Tyr Phe Ser Ile Glu
        115                 120                 125

Cys Val Leu Tyr Leu Trp Ala Leu Lys Ile Leu Tyr Pro Lys Thr Leu
    130                 135                 140

Phe Leu Leu Arg Gly Asn His Glu Cys Arg His Leu Thr Glu Tyr Phe
145                 150                 155                 160

Thr Phe Lys Gln Glu Cys Lys Ile Lys Tyr Ser Glu Arg Val Tyr Asp
                165                 170                 175

Ala Cys Met Asp Ala Phe Asp Cys Leu Pro Leu Ala Ala Leu Met Asn
            180                 185                 190

Gln Gln Phe Leu Cys Val His Gly Gly Leu Ser Pro Glu Ile Asn Thr
        195                 200                 205

Leu Asp Asp Ile Arg Lys Leu Asp Arg Phe Lys Glu Pro Pro Ala Tyr
    210                 215                 220

Gly Pro Met Cys Asp Ile Leu Trp Ser Asp Pro Leu Glu Asp Phe Gly
225                 230                 235                 240

Asn Glu Lys Thr Gln Glu His Phe Thr His Asn Thr Val Arg Gly Cys
                245                 250                 255

Ser Tyr Phe Tyr Ser Tyr Pro Ala Val Cys Glu Phe Leu Gln His Asn
            260                 265                 270

Asn Leu Leu Ser Ile Leu Arg Ala His Glu Ala Gln Asp Ala Gly Tyr
        275                 280                 285

Arg Met Tyr Arg Lys Ser Gln Thr Thr Gly Phe Pro Ser Leu Ile Thr
    290                 295                 300

Ile Phe Ser Ala Pro Asn Tyr Leu Asp Val Tyr Asn Asn Lys Ala Ala
305                 310                 315                 320

Val Leu Lys Tyr Glu Asn Asn Val Met Asn Ile Arg Gln Phe Asn Cys
                325                 330                 335

Ser Pro His Pro Tyr Trp Leu Pro Asn Phe Met Asp Val Phe Thr Trp
            340                 345                 350

Ser Leu Pro Phe Val Gly Glu Lys Val Thr Glu Met Leu Val Asn Val
        355                 360                 365

Leu Asn Ile Cys Ser Asp Asp Glu Leu Gly Ser Glu Glu Asp Gly Phe
    370                 375                 380
```

```
Asp Gly Ala Thr Ala Ala Ala Arg Lys Glu Val Ile Arg Asn Lys Ile
385                 390                 395                 400

Arg Ala Ile Gly Lys Met Ala Arg Val Phe Ser Val Leu Arg Glu Glu
                405                 410                 415

Ser Glu Ser Val Leu Thr Leu Lys Gly Leu Thr Pro Thr Gly Met Leu
            420                 425                 430

Pro Ser Gly Val Leu Ser Gly Gly Lys Gln Thr Leu Gln Ser Ala Thr
        435                 440                 445

Val Glu Ala Ile Glu Ala Asp Glu Ala Ile Lys Gly Phe Ser Pro Gln
    450                 455                 460

His Lys Ile Thr Ser Phe Glu Glu Ala Lys Gly Leu Asp Arg Ile Asn
465                 470                 475                 480

Glu Arg Met Pro Pro Arg Arg Asp Ala Met Pro Ser Asp Ala Asn Leu
                485                 490                 495

Asn Ser Ile Asn Lys Ala Leu Thr Ser Glu Thr Asn Gly Thr Asp Ser
            500                 505                 510

Asn Gly Ser Asn Ser Ser Asn Ile Gln
        515                 520
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<210> 17
<211> 2194
<212> DNA
<213> Mus musculus

<220>
<223> mouse calmodulin-dependent phosphoprotein
phosphatase catalytic subunit, calcineurin A alpha
(PPP3CA) cDNA

<220>
<221> CDS
<222> (76)..(1641)
<223> CTGF

<400> 17
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gacgcctgta tggatgcctt cgactgcctt cccctggctg cgctaatgaa ccagcagttc 660
ctgtgtgtac acggtggttt gtctccagag attaacactc tagatgacat cagaaaatta 720
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tgttcgtact tctacagtta cccagctgtg tgtgacttcc tgcagcacaa taatttgttg 900
tccatactcc gcgcccacga agcccaggat gcagggtacc gcatgtacag gaaaagccaa 960
acaacaggct tcccgtctct aattacaatc ttctcggcac caaattactt agatgtgtac 1020
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```

<210> 18
<211> 521
<212> PRT
<213> Mus musculus

<220>
<223> mouse calmodulin-dependent phosphoprotein phosphatase catalytic subunit, calcineurin A alpha (PPP3CA)

<400> 18

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Met Ser Glu Pro Lys Ala Ile Asp Pro Lys Leu Ser Thr Thr Asp Arg
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Val Val Lys Ala Val Pro Phe Pro Pro Ser His Arg Leu Thr Ala Lys
             20                  25                  30

Glu Val Phe Asp Asn Asp Gly Lys Pro Arg Val Asp Ile Leu Lys Ala
         35                  40                  45

His Leu Met Lys Glu Gly Arg Leu Glu Glu Ser Val Ala Leu Arg Ile
     50                  55                  60

Ile Thr Glu Gly Ala Ser Ile Leu Arg Gln Glu Lys Asn Leu Leu Asp
 65                  70                  75                  80

Ile Asp Ala Pro Val Thr Val Cys Gly Asp Ile His Gly Gln Phe Phe
                 85                  90                  95

Asp Leu Met Lys Leu Phe Glu Val Gly Gly Ser Pro Ala Asn Thr Arg
            100                 105                 110

Tyr Leu Phe Leu Gly Asp Tyr Val Asp Arg Gly Tyr Phe Ser Ile Glu
        115                 120                 125

Cys Val Leu Tyr Leu Trp Ala Leu Lys Ile Leu Tyr Pro Lys Thr Leu
    130                 135                 140
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Phe Leu Leu Arg Gly Asn His Glu Cys Arg His Leu Thr Glu Tyr Phe
145                 150                 155                 160

Thr Phe Lys Gln Glu Cys Lys Ile Lys Tyr Ser Glu Arg Val Tyr Asp
                165                 170                 175

Ala Cys Met Asp Ala Phe Asp Cys Leu Pro Leu Ala Ala Leu Met Asn
            180                 185                 190

Gln Gln Phe Leu Cys Val His Gly Gly Leu Ser Pro Glu Ile Asn Thr
        195                 200                 205

Leu Asp Asp Ile Arg Lys Leu Asp Arg Phe Lys Glu Pro Pro Ala Tyr
    210                 215                 220

Gly Pro Met Cys Asp Ile Leu Trp Ser Asp Pro Leu Glu Asp Phe Gly
225                 230                 235                 240

Asn Glu Lys Thr Gln Glu His Phe Thr His Asn Thr Val Arg Gly Cys
                245                 250                 255

Ser Tyr Phe Tyr Ser Tyr Pro Ala Val Cys Asp Phe Leu Gln His Asn
            260                 265                 270

Asn Leu Leu Ser Ile Leu Arg Ala His Glu Ala Gln Asp Ala Gly Tyr
        275                 280                 285

Arg Met Tyr Arg Lys Ser Gln Thr Thr Gly Phe Pro Ser Leu Ile Thr
    290                 295                 300

Ile Phe Ser Ala Pro Asn Tyr Leu Asp Val Tyr Asn Asn Lys Ala Ala
305                 310                 315                 320

Val Leu Lys Tyr Glu Asn Asn Val Met Asn Ile Arg Gln Phe Asn Cys
                325                 330                 335

Ser Pro His Pro Tyr Trp Leu Pro Asn Phe Met Asp Val Phe Thr Trp
            340                 345                 350

Ser Leu Pro Phe Val Gly Glu Lys Val Thr Glu Met Leu Val Asn Val
        355                 360                 365

Leu Asn Ile Cys Ser Asp Asp Glu Leu Gly Ser Glu Glu Asp Gly Phe
    370                 375                 380

Asp Gly Ala Thr Ala Ala Ala Arg Lys Glu Val Ile Arg Asn Lys Ile
385                 390                 395                 400

Arg Ala Ile Gly Lys Met Ala Arg Val Phe Ser Val Leu Arg Glu Glu
                405                 410                 415

Ser Glu Ser Val Leu Thr Leu Lys Gly Leu Thr Pro Thr Gly Met Leu
            420                 425                 430

Pro Ser Gly Val Leu Ser Gly Gly Lys Gln Thr Leu Gln Ser Ala Thr
        435                 440                 445

Val Glu Ala Ile Glu Ala Asp Glu Ala Ile Lys Gly Phe Ser Pro Gln
    450                 455                 460
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His Lys Ile Thr Ser Phe Glu Glu Ala Lys Gly Leu Asp Arg Ile Asn
465                 470                 475                 480

Glu Arg Met Pro Pro Arg Arg Asp Ala Met Pro Ser Asp Ala Asn Leu
                485                 490                 495

Asn Ser Ile Asn Lys Ala Leu Ala Ser Glu Thr Asn Gly Thr Asp Ser
            500                 505                 510

Asn Gly Ser Asn Ser Ser Asn Ile Gln
        515                 520
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<210> 19
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<212> DNA
<213> Rattus norvegicus

<220>
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phosphatase catalytic subunit, calcineurin A alpha
(PPP3CA) cDNA

<220>
<221> CDS
<222> (271)..(1806)
<223> PPP3CA

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(PPP3CA)

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35 40 45

His Leu Met Lys Glu Gly Arg Leu Glu Glu Ser Val Ala Leu Arg Ile
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Ile Thr Glu Gly Ala Ser Ile Leu Arg Gln Glu Lys Asn Leu Leu Asp
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85 90 95

Asp Leu Met Lys Leu Phe Glu Val Gly Gly Ser Pro Ala Asn Thr Arg
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Tyr Leu Phe Leu Gly Asp Tyr Val Asp Arg Gly Tyr Phe Ser Ile Glu
115 120 125

Cys Val Leu Tyr Leu Trp Ala Leu Lys Ile Leu Tyr Pro Lys Thr Leu
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Phe Leu Leu Arg Gly Asn His Glu Cys Arg His Leu Thr Glu Tyr Phe
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Thr Phe Lys Gln Glu Cys Lys Ile Lys Tyr Ser Glu Arg Val Tyr Asp
165 170 175

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Gln Gln Phe Leu Cys Val His Gly Gly Leu Ser Pro Glu Ile Asn Thr
195 200 205

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Gly Pro Met Cys Asp Ile Leu Trp Ser Asp Pro Leu Glu Asp Phe Gly
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Ser Tyr Phe Tyr Ser Tyr Pro Ala Val Cys Asp Phe Leu Gln His Asn
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Asp Gly Ala Thr Ala Ala Ala Arg Lys Glu Val Ile Arg Asn Lys Ile
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Arg Ala Ile Gly Lys Met Ala Arg Val Phe Ser Val Leu Arg Glu Glu
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Pro Ser Gly Val Leu Ser Gly Gly Lys Gln Thr Leu Gln Ser Ala Ile
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Lys Gly Phe Ser Pro Gln His Lys Ile Thr Ser Phe Glu Glu Ala Lys
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Gly Leu Asp Arg Ile Asn Glu Arg Met Pro Pro Arg Arg Asp Ala Met
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Pro Ser Asp Ala Asn Leu Asn Ser Ile Asn Lys Ala Leu Ala Ser Glu
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type 3 (PTPN3a) cDNA

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<223> PTPN3a

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type 3 (PTPN3a)

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Ile His Phe Leu Asp Gly Val Val Gln Thr Phe Lys Val Thr Lys Gln
35 40 45

Asp Thr Gly Gln Val Leu Leu Asp Met Val His Asn His Leu Gly Val
50 55 60

Thr Glu Lys Glu Tyr Phe Gly Leu Gln His Asp Asp Asp Ser Val Asp
65 70 75 80

Ser Pro Arg Trp Leu Glu Ala Ser Lys Pro Ile Arg Lys Gln Leu Lys
85 90 95

Gly Gly Phe Pro Cys Thr Leu His Phe Arg Val Arg Phe Phe Ile Pro
100 105 110

Asp Pro Asn Thr Leu Gln Gln Glu Gln Thr Arg His Leu Tyr Phe Leu
115 120 125

Gln Leu Lys Met Asp Ile Cys Glu Gly Arg Leu Thr Cys Pro Leu Asn
130 135 140

Ser Ala Val Val Leu Ala Ser Tyr Ala Val Gln Ser His Phe Gly Asp
145 150 155 160

Tyr Asn Ser Ser Ile His His Pro Gly Tyr Leu Ser Asp Ser His Phe
165 170 175

Ile Pro Asp Gln Asn Glu Asp Phe Leu Thr Lys Val Glu Ser Leu His
180 185 190

Glu Gln His Ser Gly Leu Lys Gln Ser Glu Ala Glu Ser Cys Tyr Ile
195 200 205

Asn Ile Ala Arg Thr Leu Asp Phe Tyr Gly Val Glu Leu His Ser Gly
210 215 220

Arg Asp Leu His Asn Leu Asp Leu Met Ile Gly Ile Ala Ser Ala Gly
225 230 235 240

Val Ala Val Tyr Arg Lys Tyr Ile Cys Thr Ser Phe Tyr Pro Trp Val
245 250 255

Asn Ile Leu Lys Ile Ser Phe Lys Arg Lys Lys Phe Phe Ile His Gln
260 265 270

Arg Gln Lys Gln Ala Glu Ser Arg Glu His Ile Val Ala Phe Asn Met
275 280 285

Leu Asn Tyr Arg Ser Cys Lys Asn Leu Trp Lys Ser Cys Val Glu His
290 295 300

His Thr Phe Phe Gln Ala Lys Lys Leu Leu Pro Gln Glu Lys Asn Val
305 310 315 320

Leu Ser Gln Tyr Trp Thr Met Gly Ser Arg Asn Thr Lys Lys Ser Val
325 330 335

Asn Asn Gln Tyr Cys Lys Lys Val Ile Gly Gly Met Val Trp Asn Pro
340 345 350

Ala Met Arg Arg Ser Leu Ser Val Glu His Leu Glu Thr Lys Ser Leu
355 360 365

Pro Ser Arg Ser Pro Pro Ile Thr Pro Asn Trp Arg Ser Pro Arg Leu
370 375 380

Arg His Glu Ile Arg Lys Pro Arg His Ser Ser Ala Asp Asn Leu Ala
385 390 395 400

Asn Glu Met Thr Tyr Ile Thr Glu Thr Glu Asp Val Phe Tyr Thr Tyr
405 410 415

Lys Gly Ser Leu Ala Pro Gln Asp Ser Asp Ser Glu Val Ser Gln Asn
420 425 430

Arg Ser Pro His Gln Glu Ser Leu Ser Glu Asn Asn Pro Ala Gln Ser
435 440 445

Tyr Leu Thr Gln Lys Ser Ser Ser Ser Val Ser Pro Ser Ser Asn Ala
450 455 460

Pro Gly Ser Cys Ser Pro Asp Gly Val Asp Gln Gln Leu Leu Asp Asp
465 470 475 480

Phe His Arg Val Thr Lys Gly Gly Ser Thr Glu Asp Ala Ser Gln Tyr
485 490 495

Tyr Cys Asp Lys Asn Asp Asn Gly Asp Ser Tyr Leu Val Leu Ile Arg
500 505 510

Ile Thr Pro Asp Glu Asp Gly Lys Phe Gly Phe Asn Leu Lys Gly Gly
515 520 525

Val Asp Gln Lys Met Pro Leu Val Val Ser Arg Ile Asn Pro Glu Ser
530 535 540

Pro Ala Asp Thr Cys Ile Pro Lys Leu Asn Glu Gly Asp Gln Ile Val
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Leu Ile Asn Gly Arg Asp Ile Ser Glu His Thr His Asp Gln Val Val
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Met Phe Ile Lys Ala Ser Arg Glu Ser His Ser Arg Glu Leu Ala Leu
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Lys Pro Gly Leu Ala Ile Thr Phe Ala Lys Leu Pro Gln Asn Leu Asp
660 665 670

Lys Asn Arg Tyr Lys Asp Val Leu Pro Tyr Asp Thr Thr Arg Val Leu
675 680 685

Leu Gln Gly Asn Glu Asp Tyr Ile Asn Ala Ser Tyr Val Asn Met Glu
690 695 700

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705 710 715 720

Leu Pro His Thr Cys Ala Gln Phe Trp Gln Val Val Trp Asp Gln Lys
725 730 735

Leu Ser Leu Ile Val Met Leu Thr Thr Leu Thr Glu Arg Gly Arg Thr
740 745 750

Lys Cys His Gln Tyr Trp Pro Asp Pro Pro Asp Val Met Asn His Gly
755 760 765

Gly Phe His Ile Gln Cys Gln Ser Glu Asp Cys Thr Ile Ala Tyr Val
770 775 780

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Ser Arg Glu Met Leu Val Thr Asn Thr Gln Thr Gly Glu Glu His Thr
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Val Thr His Leu Gln Tyr Val Ala Trp Pro Asp His Gly Ile Pro Asp
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Asp Ser Ser Asp Phe Leu Glu Phe Val Asn Tyr Val Arg Ser Leu Arg
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Val Asp Ser Glu Pro Val Leu Val His Cys Ser Ala Gly Ile Gly Arg
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Thr Gly Val Leu Val Thr Met Glu Thr Ala Met Cys Leu Thr Glu Arg
    850                 855                 860

Asn Leu Pro Ile Tyr Pro Leu Asp Ile Val Arg Lys Met Arg Asp Gln
865                 870                 875                 880

Arg Ala Met Met Val Gln Thr Ser Ser Gln Tyr Lys Phe Val Cys Glu
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Ala Ile Leu Arg Val Tyr Glu Glu Gly Leu Val Gln Met Leu Asp Pro
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Ser
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type 3 (PTPN3) cDNA

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gaccatggca tctttcacat ccagtgtcag acagaggact gtaccattgc ttacgtgtcc 2700
cgagaaatgc tagttacaaa cacggagacc ggggaagaac acacagtgac ccatctccag 2760
tatgtggcgt ggcctgacca cggcgtacct gatgactcat cagacttcct ggagtttgtg 2820
aagtatgtga ggtccctgag ggtcgacggt gagcctgccc tcgttcactg cagtgctgga 2880
ataggtcgga caggtgtttt agtcactatg gaaacagcca tgtgcttaat tgagaggaac 2940
ctgcctgttt acccactgga tattgtccgg aaaatgagag accagcgcgc gatgatggtg 3000
cagacgtcaa gccaatacaa gtttgtgtgt gaagcgatcc ttcgagtgta cgaagaaggc 3060
ttagtccaga ggctggatcc cagttag 3087

<210> 24
<211> 1028
<212> PRT
<213> Mus musculus

<220>
<223> mouse protein tyrosine phosphatase, non-receptor
type 3 (PTPN3)

<400> 24
Met Val Asn Lys Pro Arg Asp Pro Pro Pro Gln Pro Gly Ile Gln Gly
1 5 10 15

Ile Phe His Pro Ala Gln Glu Thr Pro Thr Gly Ile Pro Gly Leu Gln
20 25 30

Arg Thr Val Gly Trp Glu Tyr Glu Val Lys Gln Leu Phe Ser Gly Lys
35 40 45

Leu Ala Arg Lys Tyr Ile Pro Asp Ser Ser Asp Ile Phe Ile Glu Lys
50 55 60

Gly Met Val Glu Val Val Gly Tyr Ser Ala Ala Val Met Thr Ser Arg
65 70 75 80

```
Leu Arg Ala Leu Gly Gly Arg Ile Asn Asn Thr Arg Thr Ser Glu Leu
                85                  90                  95

Pro Lys Glu Lys Thr Arg Ser Glu Val Ile Cys Ser Ile Arg Phe Leu
            100                 105                 110

Asp Gly Leu Val Gln Thr Phe Lys Val Asn Lys Gln Asp Leu Gly Gln
        115                 120                 125

Ser Leu Leu Asp Met Ala Tyr Gly His Leu Gly Val Thr Glu Lys Glu
    130                 135                 140

Tyr Phe Gly Leu Gln His Gly Asp Asp Pro Val Asp Ser Pro Arg Trp
145                 150                 155                 160

Leu Glu Ala Ser Lys Pro Leu Arg Lys Gln Leu Lys Gly Glu Tyr Ala
                165                 170                 175

Leu Ala Ser Leu Gly Arg Trp Val Tyr Gly Lys Leu Ser Ser Pro Tyr
            180                 185                 190

Gly Gly Leu Lys Val Ala Gly Lys Pro Asn Leu Phe Leu Lys Asn Val
        195                 200                 205

Val Gly Gly Phe Pro Cys Thr Leu His Phe Arg Val Arg Tyr Phe Ile
    210                 215                 220

Pro Asp Pro Asn Thr Leu Gln Gln Glu Gln Thr Arg His Leu Tyr Phe
225                 230                 235                 240

Leu Gln Leu Lys Met Asp Val Cys Glu Gly Arg Leu Thr Cys Pro Leu
                245                 250                 255

Asn Ser Ala Val Val Leu Ala Ser Tyr Ala Val Gln Ser His Phe Gly
            260                 265                 270

Asp Phe Asn Ser Ser Ile His His Pro Gly Tyr Leu Ala Asp Ser Gln
        275                 280                 285

Phe Ile Pro Asp Gln Asn Asp Asp Phe Leu Ser Lys Val Glu Ser Leu
    290                 295                 300

His Glu Gln His Ser Gly Leu Lys Gln Ser Glu Ala Glu Ser Cys Tyr
305                 310                 315                 320

Ile Asn Ile Ala Arg Thr Leu Asp Phe Tyr Gly Val Glu Leu His Gly
                325                 330                 335

Gly Arg Asp Leu His Asn Leu Asp Leu Met Ile Gly Ile Ala Ser Ala
            340                 345                 350

Gly Ile Ala Val Tyr Arg Lys Tyr Ile Cys Thr Ser Phe Tyr Pro Trp
        355                 360                 365

Lys Lys Phe Phe Ile His Gln Arg Gln Lys Gln Glu Glu Lys Ile Val
    370                 375                 380

Ala Val Arg Ser Ser Asp Pro Val Ala Ile Ser Ala Glu Ser Arg Glu
385                 390                 395                 400
```

```
His Ile Val Ala Phe Asn Met Leu Asn Tyr Arg Ser Cys Lys Asn Leu
                405                 410                 415

Trp Lys Ser Cys Val Glu His His Ser Phe Phe Gln Ala Lys Lys Leu
            420                 425                 430

Leu Pro Gln Glu Lys Asn Val Leu Ser Gln Tyr Trp Thr Leu Gly Ser
        435                 440                 445

Arg Asn Pro Lys Lys Ser Val Asn Asn Gln Tyr Cys Lys Lys Val Ile
    450                 455                 460

Gly Gly Met Val Trp Asn Pro Val Met Arg Arg Ser Leu Ser Val Glu
465                 470                 475                 480

Arg Leu Glu Thr Lys Ser Leu Pro Ser Arg Ser Pro Pro Ile Thr Pro
                485                 490                 495

Asn Trp Arg Ser Pro Arg Leu Arg His Glu Ile Arg Lys Pro Arg His
            500                 505                 510

Ser Ser Ala Asp Asn Leu Ala Asn Glu Met Thr Tyr Ile Thr Glu Thr
        515                 520                 525

Glu Asp Val Phe Tyr Thr Tyr Lys Gly Pro Leu Ser Pro Lys Asp Ser
    530                 535                 540

Asp Ser Glu Val Ser Gln Asn His Ser Pro His Arg Glu Ser Leu Ser
545                 550                 555                 560

Glu Asn Asn Pro Ala Gln Ser Cys Leu Thr Gln Lys Ser Ser Ser Ser
                565                 570                 575

Val Ser Pro Ser Ser Asn Ala Pro Gly Ser Cys Ser Pro Asp Gly Val
            580                 585                 590

Asp Gln Arg Phe Leu Glu Asp Tyr His Lys Val Thr Lys Gly Gly Phe
        595                 600                 605

Val Glu Asp Ala Ser Gln Tyr Tyr Cys Asp Lys Ser Asp Asp Gly Asp
    610                 615                 620

Gly Tyr Leu Val Leu Ile Arg Ile Thr Pro Asp Glu Glu Gly Arg Phe
625                 630                 635                 640

Gly Phe Asn Leu Lys Ala Asp Thr Cys Met Pro Lys Leu Asn Glu Gly
                645                 650                 655

Asp Gln Ile Val Leu Ile Asn Gly Arg Asp Ile Ser Glu His Thr His
            660                 665                 670

Asp Gln Val Val Met Phe Ile Lys Ala Ser Arg Glu Ser His Ser Arg
        675                 680                 685

Glu Leu Ala Leu Val Ile Arg Arg Lys Gly Lys Ala Thr Phe Val Gly
    690                 695                 700

His Glu Gly Leu Val Pro Ala Arg Ala Val Arg Ser Leu Ala Glu Ile
705                 710                 715                 720
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Arg Ser Glu Asp Glu Leu Ser Gln Leu Phe Pro Glu Ala Met Phe Pro
                725                 730                 735

Ala Cys Pro Glu Gly Gly Asp Ser Leu Glu Gly Ser Met Glu Leu Leu
            740                 745                 750

Lys Lys Gly Leu Glu Ser Gly Thr Val Leu Ile Gln Phe Glu Gln Leu
        755                 760                 765

Tyr Arg Lys Lys Pro Gly Leu Ala Val Ser Phe Ala Lys Leu Pro Gln
    770                 775                 780

Asn Leu Asp Lys Asn Arg Tyr Lys Asp Val Leu Pro Tyr Asp Thr Thr
785                 790                 795                 800

Arg Val Leu Leu Gln Gly Asn Glu Asp Tyr Ile Asn Ala Ser Tyr Val
                805                 810                 815

Asn Met Glu Met Pro Ala Ala Asn Leu Val Asn Lys Tyr Ile Ala Thr
            820                 825                 830

Gln Gly Pro Leu Pro Asn Thr Cys Ala Gln Phe Trp Gln Val Val Trp
        835                 840                 845

Asp Gln Lys Leu Ser Leu Val Val Met Leu Thr Thr Leu Thr Glu Arg
    850                 855                 860

Gly Arg Thr Lys Cys His Gln Tyr Trp Pro Asp Pro Pro Asp Ile Met
865                 870                 875                 880

Asp His Gly Ile Phe His Ile Gln Cys Gln Thr Glu Asp Cys Thr Ile
                885                 890                 895

Ala Tyr Val Ser Arg Glu Met Leu Val Thr Asn Thr Glu Thr Gly Glu
            900                 905                 910

Glu His Thr Val Thr His Leu Gln Tyr Val Ala Trp Pro Asp His Gly
        915                 920                 925

Val Pro Asp Asp Ser Ser Asp Phe Leu Glu Phe Val Lys Tyr Val Arg
    930                 935                 940

Ser Leu Arg Val Asp Gly Glu Pro Ala Leu Val His Cys Ser Ala Gly
945                 950                 955                 960

Ile Gly Arg Thr Gly Val Leu Val Thr Met Glu Thr Ala Met Cys Leu
                965                 970                 975

Ile Glu Arg Asn Leu Pro Val Tyr Pro Leu Asp Ile Val Arg Lys Met
            980                 985                 990

Arg Asp Gln Arg Ala Met Met Val Gln Thr Ser Ser Gln Tyr Lys Phe
        995                 1000                1005

Val Cys Glu Ala Ile Leu Arg Val Tyr Glu Glu Gly Leu Val Gln Arg
    1010                1015                1020

Leu Asp Pro Ser
1025
```

<210> 25
<211> 2607
<212> DNA
<213> Homo sapiens

<220>
<223> human protein tyrosine phosphatase, non-receptor
type 3 (PTPN3b) splice variant cDNA

<220>
<221> CDS
<222> (1)..(2607)
<223> PTPN3b splice variant

<400> 25
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cccaaagaga aaactcgatc agaagtcatt tgcagcatcc acttttaga tggcgtggta 120
cagaccttta aagttactaa acaagacact ggccaggttc ttctggatat ggtgcacaac 180
cacctgggtg tgactgaaaa ggaatatttt ggtttacagc atgatgacga ctccgtggac 240
tctcctagat ggctggaagc aagcaaaccc atcaggaagc agttaaaagg aggtttcccc 300
tgtaccctgc attttcgagt aagatttttt atacctgatc ccaacacact gcagcaagaa 360
caaaccaggc acttgtattt cttacaactg aagatggata tttgcgaagg aaggttaacc 420
tgccctctta actcagcagt ggttctagcg tcctatgccg tacaatctca ttttggagac 480
tataattctt ccatacatca tccaggctat ctttccgata gtcactttat acccgatcaa 540
aatgaggact ttttaacaaa agtcgaatct ctgcatgagc agcacagtgg gctaaaacaa 600
tcagaagcag aatcctgcta tatcaacata gcgcggaccc tcgacttcta tggagtagaa 660
ctgcacagtg gtagggatct gcacaattta gacctaatga ttggaattgc ttccgcgggt 720
gttgctgtgt accgaaaata catttgcaca agtttctatc cttgggtgaa cattctcaaa 780
atttctttca aaaggaaaaa gttcttcata catcagcgac agaaacaggc tgaatccagg 840
gaacatattg tggccttcaa catgctgaat taccgatctt gcaaaaactt gtggaaatcc 900
tgtgttgagc accatacgtt ctttcaggca aagaagctac tacctcagga aaagaatgtt 960
ctgtctcagt actggactat gggctctcgg aacaccaaaa agcgaagtcc tcggctccgg 1020
cacgaaatcc gaaagccacg ccactcttct gcagataacc ttgcaaatga aatgacctac 1080
atcacggaaa cggaagatgt attttacacg tacaagggct ctctggcccc tcaagacagc 1140
gattctgaag tttctcagaa ccgaagcccg caccaagaga gtttatccga gaacaatccg 1200
gcacaaagct acctgaccca gaagtcatcc agttctgtgt ctccatcttc aaatgctcca 1260
ggctcctgct cacctgacgg cgttgatcag cagctcttag atgacttcca cagggtgacc 1320
aaaggggct ccaccgagga cgccagccag tactactgtg acaagaatga taatggtgac 1380
agctacttag tcttgatccg tatcacacca gatgaagatg gaaaatttgg atttaatctt 1440
aagggaggag tggatcaaaa gatgcctctt gtggtatcaa ggataaaccc agagtcacct 1500
gcggacacct gcattcctaa gctgaacgaa ggggatcaaa tcgtgttaat caatggccgg 1560
gacatctcag aacacacgca tgaccaagtg gtgatgttca tcaaagccag ccgggagtcc 1620
cactcacggg agctggccct ggtgatcagg aggagagctg tccgctcatt tgctgacttc 1680
aagtctgaag atgaactgaa ccagcttttc cccgaagcca ttttccccat gtgtccggag 1740
ggtggggaca ctttggaggg atccatggca cagctaaaga agggcctcga aagcgggacg 1800
gtgctgatcc agtttgagca actctacaga aaaaagccag gtttggccat cacgtttgca 1860
aagctgcctc aaaatttgga caaaaaccga tataaagatg tgctgcctta tgacaccacc 1920
cgggtattat tgcagggaaa tgaagattat attaatgcaa gttacgtgaa catggaaatt 1980
cctgctgcta accttgtgaa caagtacatc gccactcagg ggcccctgcc gcatacctgt 2040
gcacagtttt ggcaggttgt ctgggatcag aagttgtcac tcattgtcat gttgacgact 2100
ctcacagaac gagggcggac caaatgtcac cagtactggc cagatccccc cgacgtcatg 2160
aaccacggcg gctttcacat ccagtgtcag tcagaggact gcaccatcgc ctatgtgtcc 2220
cgagaaatgc tggtcacaaa cacccagacc ggggaagaac acacagtgac acatctccag 2280
tacgtcgcat ggcctgacca cggtataccc gatgactcct ccgactttct ggaatttgta 2340
aactatgtga ggtctctgag agtggacagc gagcctgtcc tagttcactg cagtgctgga 2400
ataggtcgaa ccggtgtgtt ggtcactatg gaaacagcca tgtgcctaac tgagaggaac 2460
ctgcccattt acccactgga tattgtccga aaaatgcgag accagcgcgc catgatggtg 2520
cagacatcaa gccagtacaa gtttgtgtgt gaagcgattc ttcgtgtgta tgaagaaggt 2580
ttagtccaaa tgctggatcc tagttaa 2607

<210> 26
<211> 868
<212> PRT
<213> Homo sapiens

<220>
<223> human protein tyrosine phosphatase, non-receptor
type 3 (PTPN3b) splice variant

<400> 26
Met Thr Ser Arg Leu Arg Ala Leu Gly Gly Arg Ile Asn Asn Ile Arg
1 5 10 15

Thr Ser Glu Leu Pro Lys Glu Lys Thr Arg Ser Glu Val Ile Cys Ser
20 25 30

Ile His Phe Leu Asp Gly Val Val Gln Thr Phe Lys Val Thr Lys Gln
35 40 45

Asp Thr Gly Gln Val Leu Leu Asp Met Val His Asn His Leu Gly Val
50 55 60

Thr Glu Lys Glu Tyr Phe Gly Leu Gln His Asp Asp Asp Ser Val Asp
65 70 75 80

Ser Pro Arg Trp Leu Glu Ala Ser Lys Pro Ile Arg Lys Gln Leu Lys
85 90 95

Gly Gly Phe Pro Cys Thr Leu His Phe Arg Val Arg Phe Phe Ile Pro
100 105 110

Asp Pro Asn Thr Leu Gln Gln Glu Gln Thr Arg His Leu Tyr Phe Leu
115 120 125

Gln Leu Lys Met Asp Ile Cys Glu Gly Arg Leu Thr Cys Pro Leu Asn
130 135 140

Ser Ala Val Val Leu Ala Ser Tyr Ala Val Gln Ser His Phe Gly Asp
145 150 155 160

Tyr Asn Ser Ser Ile His His Pro Gly Tyr Leu Ser Asp Ser His Phe
165 170 175

Ile Pro Asp Gln Asn Glu Asp Phe Leu Thr Lys Val Glu Ser Leu His
180 185 190

Glu Gln His Ser Gly Leu Lys Gln Ser Glu Ala Glu Ser Cys Tyr Ile
195 200 205

Asn Ile Ala Arg Thr Leu Asp Phe Tyr Gly Val Glu Leu His Ser Gly
210 215 220

Arg Asp Leu His Asn Leu Asp Leu Met Ile Gly Ile Ala Ser Ala Gly
225 230 235 240

Val Ala Val Tyr Arg Lys Tyr Ile Cys Thr Ser Phe Tyr Pro Trp Val
245 250 255

Asn Ile Leu Lys Ile Ser Phe Lys Arg Lys Lys Phe Phe Ile His Gln
260 265 270

```
Arg Gln Lys Gln Ala Glu Ser Arg Glu His Ile Val Ala Phe Asn Met
        275                 280                 285

Leu Asn Tyr Arg Ser Cys Lys Asn Leu Trp Lys Ser Cys Val Glu His
    290                 295                 300

His Thr Phe Phe Gln Ala Lys Lys Leu Leu Pro Gln Glu Lys Asn Val
305                 310                 315                 320

Leu Ser Gln Tyr Trp Thr Met Gly Ser Arg Asn Thr Lys Lys Arg Ser
                325                 330                 335

Pro Arg Leu Arg His Glu Ile Arg Lys Pro Arg His Ser Ser Ala Asp
            340                 345                 350

Asn Leu Ala Asn Glu Met Thr Tyr Ile Thr Glu Thr Glu Asp Val Phe
        355                 360                 365

Tyr Thr Tyr Lys Gly Ser Leu Ala Pro Gln Asp Ser Asp Ser Glu Val
    370                 375                 380

Ser Gln Asn Arg Ser Pro His Gln Glu Ser Leu Ser Glu Asn Asn Pro
385                 390                 395                 400

Ala Gln Ser Tyr Leu Thr Gln Lys Ser Ser Ser Ser Val Ser Pro Ser
                405                 410                 415

Ser Asn Ala Pro Gly Ser Cys Ser Pro Asp Gly Val Asp Gln Gln Leu
            420                 425                 430

Leu Asp Asp Phe His Arg Val Thr Lys Gly Gly Ser Thr Glu Asp Ala
        435                 440                 445

Ser Gln Tyr Tyr Cys Asp Lys Asn Asp Asn Gly Asp Ser Tyr Leu Val
    450                 455                 460

Leu Ile Arg Ile Thr Pro Asp Glu Asp Gly Lys Phe Gly Phe Asn Leu
465                 470                 475                 480

Lys Gly Gly Val Asp Gln Lys Met Pro Leu Val Val Ser Arg Ile Asn
                485                 490                 495

Pro Glu Ser Pro Ala Asp Thr Cys Ile Pro Lys Leu Asn Glu Gly Asp
            500                 505                 510

Gln Ile Val Leu Ile Asn Gly Arg Asp Ile Ser Glu His Thr His Asp
        515                 520                 525

Gln Val Val Met Phe Ile Lys Ala Ser Arg Glu Ser His Ser Arg Glu
    530                 535                 540

Leu Ala Leu Val Ile Arg Arg Arg Ala Val Arg Ser Phe Ala Asp Phe
545                 550                 555                 560

Lys Ser Glu Asp Glu Leu Asn Gln Leu Phe Pro Glu Ala Ile Phe Pro
                565                 570                 575

Met Cys Pro Glu Gly Gly Asp Thr Leu Glu Gly Ser Met Ala Gln Leu
            580                 585                 590
```

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Lys Lys Gly Leu Glu Ser Gly Thr Val Leu Ile Gln Phe Glu Gln Leu
        595                 600                 605

Tyr Arg Lys Lys Pro Gly Leu Ala Ile Thr Phe Ala Lys Leu Pro Gln
    610                 615                 620

Asn Leu Asp Lys Asn Arg Tyr Lys Asp Val Leu Pro Tyr Asp Thr Thr
625                 630                 635                 640

Arg Val Leu Leu Gln Gly Asn Glu Asp Tyr Ile Asn Ala Ser Tyr Val
                645                 650                 655

Asn Met Glu Ile Pro Ala Ala Asn Leu Val Asn Lys Tyr Ile Ala Thr
            660                 665                 670

Gln Gly Pro Leu Pro His Thr Cys Ala Gln Phe Trp Gln Val Val Trp
        675                 680                 685

Asp Gln Lys Leu Ser Leu Ile Val Met Leu Thr Thr Leu Thr Glu Arg
    690                 695                 700

Gly Arg Thr Lys Cys His Gln Tyr Trp Pro Asp Pro Pro Asp Val Met
705                 710                 715                 720

Asn His Gly Gly Phe His Ile Gln Cys Gln Ser Glu Asp Cys Thr Ile
                725                 730                 735

Ala Tyr Val Ser Arg Glu Met Leu Val Thr Asn Thr Gln Thr Gly Glu
            740                 745                 750

Glu His Thr Val Thr His Leu Gln Tyr Val Ala Trp Pro Asp His Gly
        755                 760                 765

Ile Pro Asp Asp Ser Ser Asp Phe Leu Glu Phe Val Asn Tyr Val Arg
    770                 775                 780

Ser Leu Arg Val Asp Ser Glu Pro Val Leu Val His Cys Ser Ala Gly
785                 790                 795                 800

Ile Gly Arg Thr Gly Val Leu Val Thr Met Glu Thr Ala Met Cys Leu
                805                 810                 815

Thr Glu Arg Asn Leu Pro Ile Tyr Pro Leu Asp Ile Val Arg Lys Met
            820                 825                 830

Arg Asp Gln Arg Ala Met Met Val Gln Thr Ser Ser Gln Tyr Lys Phe
        835                 840                 845

Val Cys Glu Ala Ile Leu Arg Val Tyr Glu Glu Gly Leu Val Gln Met
    850                 855                 860

Leu Asp Pro Ser
865
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<210> 27
<211> 861
<212> DNA
<213> Homo sapiens

<220>
<223> human dual specificity phosphatase
(tyrosine/serine), catalytic domain (DUSP3) cDNA

<220>
<221> CDS
<222> (29)..(586)
<223> DUSP3

<400> 27
gccgggcgtg cagggccccg ccgccgccat gtcgggctcg ttcgagctct cggtgcagga 60
tctcaacgac ctgctctcgg acggcagcgg ctgctacagc ctcccgagcc agccctgcaa 120
cgaggtcacc ccgcggatct acgtgggcaa cgcgtctgtg gctcaggaca tccccaagct 180
gcagaaacta ggcatcaccc atgtgctgaa cgcggctgag ggcaggtcct tcatgcacgt 240
caacaccaat gccaacttct acaaggactc cggcatcaca tacctgggca tcaaggccaa 300
cgacacacag gagttcaacc tcagcgctta ctttgaaagg gctgccgact tcattgacca 360
ggctttggct caaaagaatg gccgggtgct cgtccactgc cgggaaggtt atagccgctc 420
cccaacgcta gttatcgcct acctcatgat gcggcagaag atggacgtca agtctgccct 480
gagcatcgtg aggcagaacc gtgagatcgg ccccaacgat ggcttcctgg cccagctctg 540
ccagctcaat gacagactag ccaaggaggg gaagttgaaa ccctagggca cccccaccgc 600
ctctgctcga gaggtccgtg ggggaggccg tgggaaaggt gtccgagctg ccatgtttag 660
gaaacacact gtaccctgct cccagcatca caaggcactt gtctacaagt gtgtcccaac 720
acagtcctgg gccactttcc ccaccctggg gagcacataa agaagcttgc caaggggggc 780
gtccttgctc cccagttgtc ctgtttctgt aacttatgat gtcttttccc tgagatgggg 840
gctcagaggg ggaaggcctg t 861

<210> 28
<211> 185
<212> PRT
<213> Homo sapiens

<220>
<223> human dual specificity phosphatase
(tyrosine/serine), catalytic domain (DUSP3)

<400> 28
Met Ser Gly Ser Phe Glu Leu Ser Val Gln Asp Leu Asn Asp Leu Leu
1 5 10 15

Ser Asp Gly Ser Gly Cys Tyr Ser Leu Pro Ser Gln Pro Cys Asn Glu
20 25 30

Val Thr Pro Arg Ile Tyr Val Gly Asn Ala Ser Val Ala Gln Asp Ile
35 40 45

Pro Lys Leu Gln Lys Leu Gly Ile Thr His Val Leu Asn Ala Ala Glu
50 55 60

Gly Arg Ser Phe Met His Val Asn Thr Asn Ala Asn Phe Tyr Lys Asp
65 70 75 80

Ser Gly Ile Thr Tyr Leu Gly Ile Lys Ala Asn Asp Thr Gln Glu Phe
85 90 95

Asn Leu Ser Ala Tyr Phe Glu Arg Ala Ala Asp Phe Ile Asp Gln Ala
100 105 110

Leu Ala Gln Lys Asn Gly Arg Val Leu Val His Cys Arg Glu Gly Tyr
115 120 125

```
Ser Arg Ser Pro Thr Leu Val Ile Ala Tyr Leu Met Met Arg Gln Lys
    130                 135                 140

Met Asp Val Lys Ser Ala Leu Ser Ile Val Arg Gln Asn Arg Glu Ile
145                 150                 155                 160

Gly Pro Asn Asp Gly Phe Leu Ala Gln Leu Cys Gln Leu Asn Asp Arg
                165                 170                 175

Leu Ala Lys Glu Gly Lys Leu Lys Pro
            180                 185
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<210> 29
<211> 1196
<212> DNA
<213> Mus musculus

<220>
<223> mouse dual specificity phosphatase
(tyrosine/serine), catalytic domain (DUSP3) cDNA

<220>
<221> CDS
<222> (64)..(621)
<223> DUSP3

<400> 29
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gccatgtcca gctcgttcga actctcggtg caagatctca acgacctgct ctcggatggc 120
agcggctgct acagcctgcc gagccagccc tgcaacgagg tcgtcccgag ggtctacgtg 180
ggcaacgcgt ctgtggctca ggacatcacc cagctgcaga aactgggcat cacccacgtc 240
ctgaatgctg ccgagggcag gtccttcatg cacgtcaaca ccagtgctag cttctacgag 300
gattctggca tcacctactt gggcatcaag gccaatgata cgcaggagtt caacctcagt 360
gcttactttg aaagggccac agatttcatt gaccaggcgc tggcccataa aaatggccgg 420
gtgcttgtcc attgccgcga gggctacagc cgctccccaa cgctagttat cgcctacctc 480
atgatgcggc agaagatgga cgtcaagtct gctctgagta ctgtgaggca gaatcgtgag 540
atcggcccca acgatggctt cctggcccaa ctctgccagc tcaatgacag actagccaag 600
gagggcaagg tgaaactcta gggtgcccac agcctctttt gcagaggtct gactgggagg 660
gccctggcag ccatgtttag gaaacacagt atacccactc cctgcaccac cagacacgtg 720
cccacatctg tcccactctg gtcctcgggg gccactccac ccttagggag cacatgaaga 780
agctccctaa gaagttctgc tccttagcca tcctttcctg taatttatgt ctctccctga 840
ggtgaggttc aggtttatgt ccctgtctgt ggcatagata catctcagtg acccagggtg 900
ggagggctat cagggtgcat ggcccgggac acgggcactc ttcatgaccc ctcccccacc 960
tgggttcttc ctgtgtggtc cagaaccacg agcctggtaa aggaactatg caaacacagg 1020
ccctgacctc cccatgtctg ttcctggtcc tcacagcccg acacgccctg ctgaggcaga 1080
cgaatgacat taagttctga agcagagtgg agatagatta gtgactagat ttccaaaaag 1140
aaggaaaaaa aaggctgcat tttaaaatta tttccttaga attaaagata ctacat     1196
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<210> 30
<211> 185
<212> PRT
<213> Mus musculus

<220>
<223> mouse dual specificity phosphatase
(tyrosine/serine), catalytic domain (DUSP3)

<400> 30
Met Ser Ser Ser Phe Glu Leu Ser Val Gln Asp Leu Asn Asp Leu Leu
1 5 10 15

Ser Asp Gly Ser Gly Cys Tyr Ser Leu Pro Ser Gln Pro Cys Asn Glu
20 25 30

Val Val Pro Arg Val Tyr Val Gly Asn Ala Ser Val Ala Gln Asp Ile
35 40 45

Thr Gln Leu Gln Lys Leu Gly Ile Thr His Val Leu Asn Ala Ala Glu
50 55 60

Gly Arg Ser Phe Met His Val Asn Thr Ser Ala Ser Phe Tyr Glu Asp
65 70 75 80

Ser Gly Ile Thr Tyr Leu Gly Ile Lys Ala Asn Asp Thr Gln Glu Phe
85 90 95

Asn Leu Ser Ala Tyr Phe Glu Arg Ala Thr Asp Phe Ile Asp Gln Ala
100 105 110

Leu Ala His Lys Asn Gly Arg Val Leu Val His Cys Arg Glu Gly Tyr
115 120 125

Ser Arg Ser Pro Thr Leu Val Ile Ala Tyr Leu Met Met Arg Gln Lys
130 135 140

Met Asp Val Lys Ser Ala Leu Ser Thr Val Arg Gln Asn Arg Glu Ile
145 150 155 160

Gly Pro Asn Asp Gly Phe Leu Ala Gln Leu Cys Gln Leu Asn Asp Arg
165 170 175

Leu Ala Lys Glu Gly Lys Val Lys Leu
180 185

<210> 31
<211> 753
<212> DNA
<213> Homo sapiens

<220>
<223> human regulator of G-protein signaling 10 (RGS10)
cDNA

<220>
<221> CDS
<222> (133)..(636)
<223> RGS10

<400> 31
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atagggctcg agcggccgcc cgggcaggtg gattgttggt ctgcgtggaa cttctcaggt 120
ggacaccaga gcatggaaca catccacgac agcgatggca gttccagcag cagccaccag 180
agcctcaaga gcacagccaa atgggcggca tccctggaga atctgctgga agacccagaa 240
ggcgtgaaaa gatttaggga atttttaaaa aaggaattca gtgaagaaaa tgttttgttt 300
tggctagcat gtgaagattt taagaaaatg caagataaga cgcagatgca ggaaaaggca 360
aaggagatct acatgacctt tctgtccagc aaggcctcat cacaggtcaa cgtggagggg 420
cagtctcggc tcaacgagaa gatcctggaa gaaccgcacc ctctgatgtt ccagaaactc 480

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caggaccaga tctttaatct catgaagtac gacagctaca gccgctttct taagtctgac 540
ttgtttttaa aacacaagcg aaccgaggaa gaggaagaag atttgcctga tgctcaaact 600
gcagctaaaa gagcttccag aatttataac acatgagccc ccaaaaagcc gggactggca 660
gctttaagaa gcaaaggaat ttcctctcag gacgtgccgg gtttatcatt gctttgttat 720
ttgtaaggac tgaaatgtac aaaacccttc aat                              753
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<210> 32
<211> 167
<212> PRT
<213> Homo sapiens

<220>
<223> human regulator of G-protein signaling 10 (RGS10)

<400> 32

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Met Glu His Ile His Asp Ser Asp Gly Ser Ser Ser Ser Ser His Gln
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Ser Leu Lys Ser Thr Ala Lys Trp Ala Ala Ser Leu Glu Asn Leu Leu
             20                  25                  30

Glu Asp Pro Glu Gly Val Lys Arg Phe Arg Glu Phe Leu Lys Lys Glu
         35                  40                  45

Phe Ser Glu Glu Asn Val Leu Phe Trp Leu Ala Cys Glu Asp Phe Lys
     50                  55                  60

Lys Met Gln Asp Lys Thr Gln Met Gln Glu Lys Ala Lys Glu Ile Tyr
 65                  70                  75                  80

Met Thr Phe Leu Ser Ser Lys Ala Ser Ser Gln Val Asn Val Glu Gly
                 85                  90                  95

Gln Ser Arg Leu Asn Glu Lys Ile Leu Glu Glu Pro His Pro Leu Met
            100                 105                 110

Phe Gln Lys Leu Gln Asp Gln Ile Phe Asn Leu Met Lys Tyr Asp Ser
        115                 120                 125

Tyr Ser Arg Phe Leu Lys Ser Asp Leu Phe Leu Lys His Lys Arg Thr
    130                 135                 140

Glu Glu Glu Glu Glu Asp Leu Pro Asp Ala Gln Thr Ala Ala Lys Arg
145                 150                 155                 160

Ala Ser Arg Ile Tyr Asn Thr
                165
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<210> 33
<211> 877
<212> DNA
<213> Mus musculus

<220>
<223> mouse regulator of G-protein signaling 10 (RGS10)
cDNA

<220>
<221> CDS
<222> (60)..(605)
<223> RGS10

<400> 33
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gagatgggag ctcaagcagc ggccaccaga gccttaagag cacagccaag tgggcatcct 180
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aggacaggaa gcagatgcag gaaaaggcca aggagatcta catgaccttc ctgtccaata 360
aggcctcttc acaagtcaac gtggaggggc agtctcggct cactgaaaag attctggaag 420
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cataagctga gcccttcacc ccagcgaagg agagggatgg actcttagga ctgtacaggc 660
tgtcatttct ttgttgtgtt tgaggactgg agtgtgctag accttccctc tggatatgtg 720
tattttatta actgaacagc aacctctgca tgatgctaat cttccattaa aaacaaaagt 780
agctttaaag tgtcagttca caaaaacaca tgagattctg ccaatactgg acactcagcc 840
tttcaatcct gattaaagtg ttcgtgaagc tacaagc 877

<210> 34
<211> 181
<212> PRT
<213> Mus musculus

<220>
<223> mouse regulator of G-protein signaling 10 (RGS10)

<400> 34
Met Phe Thr Arg Ala Val Ser Arg Leu Ser Arg Lys Arg Pro Pro Ser
1 5 10 15

Asp Ile His Asp Gly Asp Gly Ser Ser Ser Ser Gly His Gln Ser Leu
20 25 30

Lys Ser Thr Ala Lys Trp Ala Ser Ser Leu Glu Asn Leu Leu Glu Asp
35 40 45

Pro Glu Gly Val Gln Arg Phe Arg Glu Phe Leu Lys Lys Glu Phe Ser
50 55 60

Glu Glu Asn Val Leu Phe Trp Leu Ala Cys Glu Asp Phe Lys Lys Thr
65 70 75 80

Glu Asp Arg Lys Gln Met Gln Glu Lys Ala Lys Glu Ile Tyr Met Thr
85 90 95

Phe Leu Ser Asn Lys Ala Ser Ser Gln Val Asn Val Glu Gly Gln Ser
100 105 110

Arg Leu Thr Glu Lys Ile Leu Glu Glu Pro His Pro Leu Met Phe Gln
115 120 125

Lys Leu Gln Asp Gln Ile Phe Asn Leu Met Lys Tyr Asp Ser Tyr Ser
130 135 140

Arg Phe Leu Lys Ser Asp Leu Phe Leu Lys Pro Lys Arg Thr Glu Glu
145 150 155 160

Glu Glu Glu Glu Pro Pro Asp Ala Gln Thr Ala Ala Lys Arg Ala Ser
165 170 175

Arg Ile Tyr Asn Thr
180

<210> 35
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hexahistidine (His) affinity tag

<400> 35
His His His His His His
1 5

<210> 36
<211> 200
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:poly-Gly flexible linker

<220>
<221> MOD_RES
<222> (6)..(200)
<223> Gly residues from position 6 to 200 may be present or absent

<400> 36
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
1 5 10 15

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
20 25 30

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
35 40 45

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
50 55 60

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
65 70 75 80

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
85 90 95

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
100 105 110

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
115 120 125

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
130 135 140

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
145 150 155 160

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
165 170 175

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
180 185 190

Gly Gly Gly Gly Gly Gly Gly Gly
195 200